

Figure 1A

1 TAGTTCTAGATCGCGAGCGGCGCGCGCGGGCCGAGGAGGGAGGAAGGAAGGAAGG 60

61 CTGGAAGGAAGGAAGCCAGGAAGAAAGAAAGGAAGGAAGGCAAGAAGGAAGGCGG 120

121 GCGGCGGGCGAGGGCGCGGGGGCCGAGCGGAGCGGGCGCGAGGCGAGGAGCGAGCGG 180

181 CCCCCCAGCACCACCGCGCGCTGCGGAAGCCCTCCCAACCCAGGAGCCGGGGAGG 240

241 GGGGAGAGCGCGAGAGGCTCCAGGCCCGCGCGAGCCCGCCCCCGCGCTCCCCGAG 300

301 CGGGCCTTGACCCCAAATTCCTGAGCCTCATTGGGGGGTCTCCCCCACGGGCCGGG 360

361 CATGCTGCCCCCCGGAAGGAACCCCTCTCTCGCTCACGATCTCGACAGGAAGCCCTGGA 420

421 GAACTGGGAGGCGAGAGACCCCGCTGGCGGAGGCGATGTGGAGGGGGGGCGCTGGCGC 480

481 AGGGAGAGGCCACGCGAAGCCAAGCCACAGGCCCCCCACGCTCCACGCGAGCATGAA 540

541 CATTGAGGATGGCGGCTGCCCGCGGCTCCCGTGCCTCCCGCTGCCCGCCGGTAGGATGT 600  
1 M A R A R G S P C P P L P P P G R M S 18

601 CCTGGCCCCACGGGGCATTGCTCTTCTCTGGCTCTTCTCCCCACCCCTGGGGCCGGTG 660  
19 W P H G A L L F L W L F S P P L G A G G 38

661 GAGGTGGAGTGGCCGTGACCTCTGCCGCGGAGGGGGCTCCCCCGCGGCCACCTCCTGCC 720  
39 G G V A V T S A A G G G S P P A T S C P 58

721 CCGTGGCGTCTCTCTGCAGCAACAGGCCAGCGGGTGATCTGCACACGGAGAGACCTGG 780  
59 V A C S C S N Q A S R V I C T R R D L A 78

781 CCGAGGTCCACGCGAGCATCCCGGTCAACACGCGGTACCTGAACCTGCAAGAGAAGCGCA 840  
79 E V P A S I P V N T R Y N Q E N G I 98

841 TCCAGGTGATCCGGACGGACAGTTCAAGACCTGCGGCACCTGGAGATTCTGCAGCTGA 900  
99 Q V I R T D T F K H L R H L E I Q S 118

901 GCAAGAACCTGGTGCACAAGATCGAGGTGGCGCGCTTCAACGGGCTGCCGACCTCAACA 960  
119 K N L V R K I E V G A F N G P S N T 138

961 CGTGAGGAGCTTTTGGACAACCGGCTGACCACGGTGCCCAACGAGGCTTCGAGTACCTGT 1020  
139 L E L F D N R L T T V P T Q A F E Y L S 158

Figure 1B

|      |  |      |
|------|--|------|
| 1021 | CCAAGCTGCGGGAGCTCTGGCTGCGGAACAACCCCATCGAGAGCATCCCCCTCTACGCCT | 1080 |
| 159  | K R E L W R N N P I E S I P S Y A F                          | 178  |
| 1081 | TCAACCGCGTGCCTCGCTGCGGCGCCTGGACCTGGGCGAGCTCAAGCGGCTGGAATACA  | 1140 |
| 179  | N R V P S R R D G E L K R L E Y I                            | 198  |
| 1141 | TCTCGGAGGCGGCCTTCGAGGGGCTGGTCAACCTGCGCTACCTCAACCTGGGCATGTGCA | 1200 |
| 199  | S E A A F E G L V N L R Y N L G M C N                        | 218  |
| 1201 | ACCTCAAGGACATCCCAACCTGACGGCCCTGGTGCCTGGAGGAGCTGGAGCTGTGCG    | 1260 |
| 219  | L K D I P N L T A L V R L E E L E S G                        | 238  |
| 1261 | GCAACCGGCTGGACCTGATCCGCCGGGCTCCTTCCAGGGTCTCACCAGCCTGGCGCAAGC | 1320 |
| 239  | N R L D L I R P G S F Q G L T S L R K L                      | 258  |
| 1321 | TGTGGCTCATGCACGCCAGGTAGCCACCATCGAGCGCAACGCCTTCGACGACCTCAAGT  | 1380 |
| 259  | W L M H A Q V A T I E R N A F D D L K S                      | 278  |
| 1381 | CGCTGGAGGAGCTCAACCTGTCCACAACAACCTGATGTGCTGCCCCACGACCTCTTCA   | 1440 |
| 279  | L E E L N L S H N N L M S L P H D L F T                      | 298  |
| 1441 | CGCCCCGACCGCCTCGAGCGGTGCACCTCAACCACAACCCCTGGCATTGCAACTGGC    | 1500 |
| 299  | P L H R L E R V H L N H N P W H C N C D                      | 318  |
| 1501 | ACGTGCTCTGGCTGAGCTGGTGGCTCAAGGAGACGGTGCCCGCAACACGACGTGTGCG   | 1560 |
| 319  | V L W L S W W L K E T V P S N T T C C A                      | 338  |
| 1561 | CCCGCTGTATGCGCCCGCGCCTCAAGGGGCGCTACATTGGGGAGCTGGACCACTCGC    | 1620 |
| 339  | R C H A F A G K G R Y I G E L D Q S H                        | 358  |
| 1621 | ATTTCACTGTCTATGCGCCCGTCATCGTGGAGCCGCCACGGACCTCAACGTACCGGAGG  | 1680 |
| 359  | F T C Y A P V I V E F P T D L N V T E G                      | 378  |
| 1681 | GCATGGCTGCCGAGCTCAAATGCGGCACGGGCACCTCCATGACCTCCGTCAACTGGCTGA | 1740 |
| 379  | M A A E L K C R T G T S M T S V N W L T                      | 398  |
| 1741 | CGCCCAACGGCACCCCTCATGACCCACGGCTCCTACCGGTGCGCAITCTCCGTCTGCTG  | 1800 |
| 399  | P N G T L M T H G S Y R V R I S V L H D                      | 418  |
| 1801 | ACGGCACGCTTAACCTTACCAACGTACCGTGCAGGACACGGGCCAGTACAGTGCATGG   | 1860 |
| 419  | G T L N F T N V T V Q D T G Q Y T C M V                      | 438  |
| 1861 | TGACGAACTCAGCCGGCAACACACCGCCTCGGCCACGCTCAACGTCTCGGCCGTGGACC  | 1920 |
| 439  | T N S A G N T T A S A T L N V S A V D P                      | 458  |

|      |  |      |
|------|--|------|
| 1921 | CCGTGGCGGCCGGGGGCACCGGCAGCGCGCGGGGCGCGCCCTGGGGGCAGTGGTGGTGTG   | 1980 |
| 459  | V A A G G T G S G G G G P G G S G G V G                        | 478  |
| 1981 | GAGGGGGCAGTGGCGGCTACACCTACTTCAACCAGGTGACCGCTGGAGACCTGGAGACGC   | 2040 |
| 479  | G G S G G Y T Y F T T V T V E T L E T Q                        | 498  |
| 2041 | AGCCCCGAGAGGAGGCCCTGCAGCCGCGGGGGACGGAGAGGAACCCGACAGGCCCCACGA   | 2100 |
| 499  | P G E E A L Q P R G G T E K E P P G P T T                      | 518  |
| 2101 | CAGACGGTGTCTGGGTGGGGGCCGGCTGGGGACGCGGCCGGCCCTGCCTCGTCTTCTA     | 2160 |
| 519  | D G V W G G G R P G D A A G P A S S S T                        | 538  |
| 2161 | CCACGGCACCCGCCCGCGCTCTCGCGGCCACGGAGAAGCGGTTACAGGTGCCCATCA      | 2220 |
| 539  | T A P A P R S S R P T E K A F T V P I T                        | 558  |
| 2221 | CGGATGTGACGGAGAAGCCCTCAAGGACCTGGACGACGTCATGAAGACCACAAAATCA     | 2280 |
| 559  | D V T E N A L K D L D D V M K T T K I I                        | 578  |
| 2281 | TCATCGGCTGCTTCGTGGCCATCACGTTTCATGGCCGGTGATGCTCGTGGCCTTCTACA    | 2340 |
| 579  | I G C F V A I T F M A A V M L V A F Y K                        | 598  |
| 2341 | AGCTGCGCAAGCAGCACCAAGCTCCACAAGCACCCAGGGCCCAACGCGCACCGTGGAGATCA | 2400 |
| 599  | L R K Q H Q L H K H H G P T R T V E I I                        | 618  |
| 2401 | TCAACGTGGAGGACGAGCTGCCCGCCCTCGGCCGTGTCCTGGGCGGCC               | 2450 |
| 619  | N V E D E L P A S A V S V A A                                  | 634  |

```

MARARSGPCPPLEP
                                :MLNKNTLHP
MSGIGWQTLSLSLALVLSLTLNKVAPHACPAQCSGSGTVDCGHGLRLIVE

PGRMNSWPHGALLFLNLFSPLGAGGGGVAVTSAGGSGS--PPATSCPVACS
QQIMIGPR----FNRLDFLIVLVLALQLQLLVAG--LVRAQTCSFVCS
                                :MARRLKLSLGLLASLL----PALAACQPNCH
RNIPNTRTFLDLNGNNTIRITTKTDFAGLRLHLRLQIMENKSTIERGAFH
                                :      :      :      :      :      :      :
CSNQASRVICTRDLRAVSPAS----IPVNTRYLNLQENQIQVIRITDFKHL
CSNQPSKVICTVRNNRLRVDKPG----ISTNRLNLHNQENQIQVSKNSFKHL
CHSDLOHVICTOKVGLQPIK----VSEKTKLNLNLRNNFPVLVATNSFRAM
DLKELERLRLNRRNQLQFPPELLFTGAKLRLVLSLNSNQIQAIPKRAFGR
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RHLTSLQLSKMLVKRIEYGAFCNGLPSLNTLELFNRLATVTPQAFEYLSK
RHLTQLSKSNHRIITEIGAFNGLANLTLELFNRLATITWGAFLYSK
PNIHLSLQHQICQREVAAGFAGLQGLLYLYLSHIDTIRVLRAQAGADFTL
VDKNLQLDQYQSTCEDEGAFRLRDLVEITLNNNNIRVSPASFNHMK
.: : * : . : : * : * : * : * : * : * : * : * : * : * :
LREL-----WLNR-----
LREL-----WLNR-----
LTYL-----YLDH-----
LRTFLRHSNNILYCDCHLANLSDNLRRPQVGLTYQCMGFSHLRGHNVAEV
* : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QKREVCSDDEEGHQSFAPSGCSVLHCPACTCSNNIVCDRGKGLTEIPT
                                :      :      :      :      :      :      :
-----NFIESIPSYAFNVRYSRLRLDELKLR-----
-----NFIESIPSYAFNKRISRLRLDELKLR-----
-----NRTFLPGLSLNLYLQGLQNNK-----
LNPLETITETRLQNSIRIVIPGASPYKRLRLDLSDNQISLAPDAFQG
* : * : * : * : * : * : * : * : * : * : * : * : * :
-----LEYISEAAFEGSLVNYRLYMLNACMNKDIP--NLTAIV--
-----LEYISGAFOGSLNRYLMLACNLRIP--NLTLPI--
-----TRELRSAGQAKDLRWLYLSNLSLSLQGLADFL--
LRSLSNLVLYGNKITLPKSLPEGLYSQLLLMLANKINCLRVDAFDQGLR
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RLEELLSGNRLDLTPSGQGLTSLRKLMMHAAQVATITERNAFDGLSL
LKLDELDSGNHLSATPSGQGLMHQKLMMTQSOQVTERNAFNQGLSL
LNAFLYLRDQYSGSPSAALSRLRVEELKLSHNPFKLSQPNAFSGPRY
LSNLSVLVLYGNKITLPKSLPEGLYSQLLLMLANKINCLRVDAFDQHLNL
* : * : * : * : * : * : * : * : * : * : * : * : * :
RLELINSN--NLMSLPDHLFTPLHLRLERVNLHNPNHNCNDVLMWSLWKE
VEYNLANL--NLTLPHDLFTPLHLHLRLHLHNPNHNCNDILMWSLWIKD
LETLMDLNTLQKYSOGAFLVGLTQTHLVLHNLNHLQNSPNFPLSDSLT
LKLSLSYN--LQYVAKGTFSAIRAQITQWHLAQNPFTDCCHLKNLADLYLT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
TPVSNITTCARCHAPAGKLGRIYELDQSHFTCYAPVIVEPPTDLNVTBG
APVSNITACCARNCTPNELKRGYIGELDQSHFTCYAPVIVEPPADNLVTEG
DLTNNPMKCT--QLRGL--LRWLAEKTSRPDATCAKCFRFG----CHIRD
PQ--IETSGARQSPRLANLRQIKQISKSKFCSGTEDYSKLSGQCDFA
.: * : * : * : * : * : * : * : * : * : * : * : * :
MAELKCKCTGTSMSVNNLTPTNGTLTGGHSYRVRISVLHDTGNFTNNTV
MAELKCRASLTSVSWITFPNGTWTHGAYKVRIVASLDGTINFTNTVTV
DIFKCTCTPKRSKAGRI-----
LACPEKRCRGGTIVDCSQQKLNKIPDITPQYTAEFLRN-----NNEETVL
.: * : * : * : * : * : * : * : * : * : * : * : * :

```

Figure 2B

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS-1  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

QDTGQYTCMVINSAGNTTASATLNVSADVPVAAAGGTSGGGGPGSGGGVGVG  
QDTGMYTCMVNSVGNNTASATLNVT-----AAT-----TT  
-----  
EATGIFKKLPQLRKINLSNNKITDIEEGAFEGASG-----VN  
: : . : . .

GGSGGYTYFTTVTVETLETQPCBEALQPRTEKEFPFGFTTDDGVWGGGRPG  
P----FSYFSTVTVETMEFSQCE----ARTDDN-VGPTPVVDN-----  
-----  
EILLTNSRLENVQHKMFGLSRLKTLMLRSNRISCVG-NDSFTGLGSRVL  
: : : . .

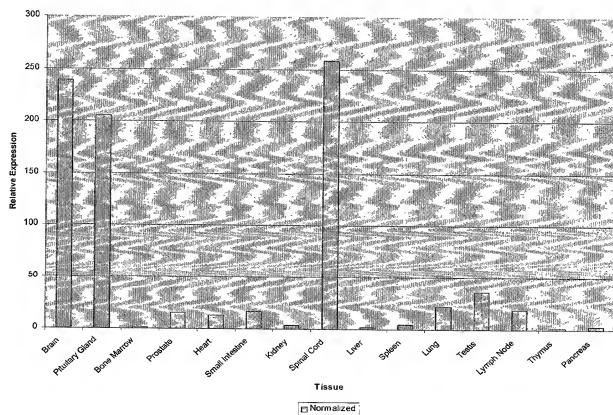
DAAGPASSSTTAPAPRSSRPTKEAFTVPITDVTEN-ALKDLDDVMKTTKI  
----ETTNVTTSLTFQSTRSTERTFTIPVTDINS--GIPGIDEVMKTTKI  
-----  
LSLYDNQITTVAPGAFGTLHSLSTLNLLANFFNCHLAMEWLKRRKI  
 . : : . .

IIG---CFVAITFMAAVMLVAFYKLRKQHOLKHHGPTRTVEIINVEDEL  
IIG---CFVAITLMAAVMLVIFVKMRKQHHRRQNHAPTRIVEIINVDDEI  
-----  
VTGNFRQCKPYFLKEIPIQDVAIQDFTCDDGNDNDSNCSPLSRCPSECTCL  
: . . . . .

PAASAVSVAA-----  
TGDTPMESHLPKPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSSVHEPL  
-----  
DTVVRCSNKGLKVLPGKIPRDVTELYDGNQFTLVPEFPFFFFFLSIF  
 .

-----  
LIRMSKDNVQETQI-  
-----  
FLFETGSGGVASALEY

Figure 3



10020392.122001

[illegible]

Figure 5B

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

HLRRNS\_1\_FL  
KIAA1580  
BOVIN\_CHONDROADHERIN\_PRECURSOR  
SLIT-2.

TVETLETQPGEEALQPRGTEKEPPGPTTDGVWGGRPGDAAGPASSSTTA  
TVETME--PSQD--EARTTDNN-VGPTTPVVDV-----ETTNVTTS  
-----  
KLNKIPDHPQYTAELRLNNEFTVLEATGIFKKLPQLRKRLNLSNNKITD  
: . : . : . : .

PAP----RSSRPTKEAFTVPITDVTEALKDLDVMKTKKII---IGCF-  
LTF-----QSTRSTETFTIPVTDINS-GLPGIDEVMKTKKII---IGCF-  
-----  
IEGAFEGASGVNEILLTSNRLNVQHRMFKGLESKLTMLRSNRISCVG  
: : . : .

-VAITFMAAVMLVAFYKLRKQHLKHGGHPTRTVEIINVEDELPAASAVS  
-VAITLMAAVMLVIFYKMRKQHHRQNHAPTRTVEIINVDDEI---T---  
-----  
NDSFTGLGSVRLLSLYDNQITTVAPGAGFTLHSLSTLMLLAMPFNCNCHL  
\* \* \* \* \*

VAAAAAV---ASGGGVGGDSHLALPALERDHLNHHHYVAA----AFKA  
-----GDTPMESHLPMPAIEHEHLNHYN-----SYKS  
-----  
AMLGEWLRRKRIVTGNPRCQKPYFLKEIPIQDVAIQDFTCDGNDNNSCS  
: . : .

HYSSNFSGGCGGKGPPLNSIHEPLLFKSGSKENVQETQI-----  
PENHTTTVNTIN--SIH--SSVHEPLLRNMNSKDNVQETQI-----  
-----  
PLSRCPSECTCLDTVVR--CSNKGKLVLPKGIIPRDVTELYLDGNQFTLV  
\* \* \* \*

-----  
-----  
EFPFFFFFFFLSIFFLFETGSGGVASALEY

10026333-12004



Figure 4A

|     |   |      |
|-----|---|------|
| 1   | CCACGCGTCCGACTAGTCTCTAGATCGCAGCGCGCCGGCGGGCCCGAGGAGGAGGAAG    | 60   |
| 61  | GAAGGAAGGAAGGCTGGAAGGAAGGAAGCCAGGAAAGAAAGAAAGAAAGGAAGGCA      | 120  |
| 121 | AGAAGGAAGCGCGGCGCGGCGAGGGCGCGGGCCCGGACGGCAGGCGGGCGCGAGGCGCA   | 180  |
| 181 | GGAGGCAGAGCGGCCCCCAGCCCCACCGCCCGCTGGCGGAAGCCCCCTCCCCACCCA     | 240  |
| 241 | GGAGCCGGGGAGGGGGGAGAGCGCGAGAGGCTCCAGGCCCCGGCCGAGCCCCGCCCCCG   | 300  |
| 301 | CGCCTCCCCCGCAGCGGGCCTTGCACCCCAAATTCCTGAGCCTCATTTGGGGGGTCTCTCC | 360  |
| 361 | CCCACGGGCGGGCATGCTGCCCCCGGAAGGAACCCCTCTCTCGCTCAGCATCTCGAC     | 420  |
| 421 | AGGAAGCCCTGGAGAACTGGGGAGGAGAGACCCCGGCTGGCCGGAGGCATGTGGAGGGG   | 480  |
| 481 | GGGGCCTGGGCGCAGGGAGAGGCCAGCGGAAGCCAAGCCACCAGGCCCCCGAGCGTCCA   | 540  |
| 541 | CGCGGAGCATGAACATTGAGGATGGCGCGTGGCCCGGCTCCCCGTCGCCCCCGCTGCCG   | 600  |
| 1   | <u>M A R A R G S P C P P L P</u>                              | 13   |
| 601 | CCCGGTAGGATGTCTGGCCCCACGGGGCATTGCTCTTCTCTGGCTCTTCTCCCCACCC    | 660  |
| 14  | <u>P G R M S W P H G A L L F L W L F S P P</u>                | 33   |
| 661 | CTGGGGCCGGTGGAGGTGGAGTGGCCGTGACGTCTGCCCGGAGGGGGCTCCCCGCGC     | 720  |
| 34  | <u>通 G A G G G G V A V T S A A G G G S P P</u>                | 53   |
| 721 | GCCACCTCTGCCCGTGGCCTGCTCCTGCAGCAACCAGGCCAGCGGGTGATCTGCACA     | 780  |
| 54  | <u>A T S C P V A C S C S N Q A S R V I C T</u>                | 73   |
| 781 | CGGAGAGACCTGGCCGAGGTCCCAGCCAGCATCCCGGTCAACACGCGGTACCTGAACCTG  | 840  |
| 74  | <u>R R D 通 A E V P A S I P V N T R Y L N 通</u>                | 93   |
| 841 | CAAGAGAAGCGCATCCAGGTGATCCGGACGGACAGTTCAGCACCTCGCGCACCTGGAG    | 900  |
| 94  | <u>Q E N G I Q V I R T D T F K H L R H L E</u>                | 113  |
| 901 | ATTCTGCAGCTGAGCAAGAACTGGTGCGCAAGATCGAGGTGGGCGCCTTCAACGGGCTG   | 960  |
| 114 | <u>I 通 Q L S K N L V R K I E V G A F N G L</u>                | 133  |
| 961 | CCCAGCCTCAACACGCTGGAGCTTTTGACAACCGGCTGACCCAGGTGCCACGCAGGCC    | 1020 |
| 134 | <u>P S L N T 通 E 通 F D N R L T T V P T Q A</u>                | 153  |

10026332.120201

Figure 4B

|      |  |      |
|------|--|------|
| 1021 | TTCGAGTACCTGTCCAAGCTGCGGGAGCTCTGGCTGCGGAACAACCCCATCGAGAGCATC | 1080 |
| 154  | F E Y L S K R E L W L R N N P I E S I                        | 173  |
| 1081 | CCCTCCTAGCCCTTCAACCGCGTGCCCTCGCTGCGGCGCCTGGACCTGGGCGAGCTCAAG | 1140 |
| 174  | P S Y A F N R V P S R R D G E L K                            | 193  |
| 1141 | CGGCTGGAATACATCTCGGAGGCGGCCTTCGAGGGGCTGGTCAACCTGCGCTACCTCAAC | 1200 |
| 194  | R L E Y I S E A A F E G L V N R Y N                          | 213  |
| 1201 | CTGGGCATGTGCAACCTCAAGGACATCCCCAACCTGACGGCCCTGGTGCGCTGGAGGAG  | 1260 |
| 214  | G M C N L K D I P N L T A L V R E E                          | 233  |
| 1261 | CTGGAGCTGTGCGGCAACCGGCTGGACCTGATCCGCCCGGGCTCCTTCCAGGGTCTCACC | 1320 |
| 234  | L E L S G N R L D L I R P G S F Q G L T                      | 253  |
| 1321 | AGCCTGCGCAAGCTGTGGCTCATGCACGCCAGGTAGCCACCATCGAGCGCAACGCCTTC  | 1380 |
| 254  | S L R K W L M H A Q V A T I E R N A F                        | 273  |
| 1381 | GACGACCTCAAGTCGCTGGAGGAGCTCAACCTGTCCCACAACACCTGATGTGCTGCCC   | 1440 |
| 274  | D D L K S L E E L N L S H N N M S L P                        | 293  |
| 1441 | CACGACCTTTCACGCCCTGCACCGCTCGAGCGGTGCACCTCAACACAAACCCCTGG     | 1500 |
| 294  | H D L F T P L H R L E R V H N H N P W                        | 313  |
| 1501 | CATTGCAACTGCGACGTGCTCTGGCTGAGCTGGTGGCTCAAGGAGACGGTGCCAGCAAC  | 1560 |
| 314  | H C N C D V L W L S W W L K E T V P S N                      | 333  |
| 1561 | ACGACGTGTGCGCCCGCTGTATGCGCCCGCGGCTCAAGGGCGCTACATTGGGGAG      | 1620 |
| 334  | T T C C A R C H A P A G K G R Y I G E                        | 353  |
| 1621 | CTGGACCAGTCGCATTTACCTGCTATGCGCCCGTCATCGTGAGCGGCCACGGACCTC    | 1680 |
| 354  | L D Q S H F T C Y A F V I V E P P T D L                      | 373  |
| 1681 | AACGTACCGAGGGCATGGCTGCCGAGCTCAAATGCCGCACGGGCACCTCCATGACCTCC  | 1740 |
| 374  | N V T E G M A A E L K C R T G T S M T S                      | 393  |
| 1741 | GTCAACTGGCTGACGCCCAACGGCACCTCATGACCCACGGCTCCTACCGCGTGCGCATC  | 1800 |
| 394  | V N W L T P N G T L M T H G S Y R V R I                      | 413  |
| 1801 | TCCGTCCTGCATGACGGCAGCTTAACTTCACCAACGTACCGTGAGGACACGGGCCAG    | 1860 |
| 414  | S V L H D G T L N F T N V T V Q D T G Q                      | 433  |
| 1861 | TACACGTGATGGTGACAACTCAGCGGCAACACCACCGCTCGGCCACGCTCAACGTC     | 1920 |
| 434  | Y T C M V T N S A G N T T A S A T L N V                      | 453  |

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Figure 4C

1921 TCGGCCGTGGACCCCGTGGCGGCCGGGGGCACCGGCAGCGCGGGGGCGGCCCTGGGGGC 1980  
 454 S A V D P V A A G G T G S G G G G P G G 473

1981 AGTGGTGGTGTGGAGGGGGCAGTGGCGGCTACACCTACTTCCACCGGTGACCGTGGAG 2040  
 474 S G G V G G G S G G Y T Y F T T V T V E 493

2041 ACCCTGGAGACGCAGCCCCGAGAGGAGGCCCTGCAGCCGCGGGGGACGGAGAAGGAACCG 2100  
 494 T L E T Q P G E E A L Q P R G T E K E P 513

2101 CCAGGGCCACGACAGACGGTGTCTGGGGTGGGGCGCGCTGGGGACGCGCGGCCCT 2160  
 514 P G P T T D G V W G G G R P G D A A G P 533

2161 GCCTGCTCTTCTACACCGGCACCCGCCCGCTCCTCGGGCCACGGAGAAGCGTTC 2220  
 534 A S S S T T A P A P R S S R P T E K A F 553

2221 ACGGTGCCCATCAGGATGTGACGGAGAAGCCCTCAAGGACCTGGACGACGTCATGAAG 2280  
 554 T V P I T D V T E N A L K D L D D V M K 573

2281 ACCACCAAATCATCATCGGCTGCTTCGTGGCCATCACGTTTCATGGCCGCGGTGATGCTC 2340  
 574 T T K I I I G C F V A I T F M A A V M L 593

2341 GTGGCCTTCTACAAGCTGCGCAAGCAGCACAGCTCCACAAGCACCGGGCCACGCGC 2400  
 594 V A F Y K L R K Q H Q L H K H H G P T R 613

2401 ACCGTGGAGATCATCAACGTGGAGGACGAGCTGCCCGCCGCTCGGCCGTGTCGTGGCC 2460  
 614 T V E I I N V E D E L P A A S A V S V A 633

2461 GCCCGGCCCGCTGGCCAGTGGGGGTGGTGGGGGGGACAGCCACCTGGCCCTGGCC 2520  
 634 A A A A V A S G G G V G G D S H L A L P 653

2521 GCCCTGGAGCGAGACCACCTCAACCACCACCACTACGTGGCTGCCGCCTTCAAGGCGCAC 2580  
 654 A L E R D H L N H H H Y V A A A F K A H 673

2581 TACAGCAGCAACCCAGCGCGGGGGGCTGCGGGGGCAAAGGCCCGCTGGCCTCAACTCC 2640  
 674 Y S S N P S G G G C G G K G P P G L N S 693

2641 ATCCACGAACCTCTGCTCTTCAAGAGCGGCTCCAAGGAGACGTGCAAGAGACGAGATC 2700  
 694 I H E P L L F K S G S K E N V Q E T Q I 713

2701 TGAGGCGGGGGCGGGCGAGGGGCGTGGAGCCCCCACCAGTCCCAGC 2756

1026392.122001

Figure 6.

**HLRRS11 (SEQ ID NO:2)**

| <b>Protein</b>                  | <b>Genbank ID</b> | <b>Identities</b> | <b>Similarities</b> |
|---------------------------------|-------------------|-------------------|---------------------|
| bovine chondroadherin precursor | gi 627724         | 32.3%             | 37.4%               |
| rat slit-2                      | gi 6579191        | 26.7%             | 33.8%               |
| KIAA1580                        | gi 10047235       | 73.9%             | 65.5%               |

**HLRRS11 (SEQ ID NO:35)**

| <b>Protein</b>                  | <b>Genbank ID</b> | <b>Identities</b> | <b>Similarities</b> |
|---------------------------------|-------------------|-------------------|---------------------|
| bovine chondroadherin precursor | gi 627724         | 32.3%             | 37.4%               |
| rat slit-2                      | gi 6579191        | 26.7%             | 33.8%               |
| KIAA1580                        | gi 10047235       | 68.0%             | 75.5%               |

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